



#4 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/039,847A

DATE: 07/02/2002

TIME: 10:15:46

Input Set : A:\00-100.txt

Output Set: N:\CRF3\07022002\J039847A.raw

ENTERED

3 <110> APPLICANT: Hart, Charles E.
4 Topouzis, Stavros
6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
7 KIDNEY FUNCTION
9 <130> FILE REFERENCE: 00-100
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/039,847A
C--> 11 <141> CURRENT FILING DATE: 2002-06-17
11 <150> PRIOR APPLICATION NUMBER: US 60/244,479
12 <151> PRIOR FILING DATE: 2000-10-30
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1882
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (226)...(1338)
27 <400> SEQUENCE: 1
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29 gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg 120
30 cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac 180
31 ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc 237
32 Met His Arg Leu
33 1
35 atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac 285
36 Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
37 5 10 15 20
39 act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc 333
40 Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
41 25 30 35
44 aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga 381
45 Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
46 40 45 50
48 gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga 429
49 Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
50 55 60 65
52 ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac 477
53 Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
54 70 75 80
56 tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga 525
57 Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
58 85 90 95 100

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60	tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt	573
61	Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	
62	105 110 115	
64	gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga	621
65	Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	
66	120 125 130	
68	cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
69	His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
70	135 140 145	
72	atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
73	Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
74	150 155 160	
76	att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765
77	Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	
78	165 170 175 180	
80	acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813
81	Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	
82	185 190 195	
84	tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861
85	Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	
86	200 205 210	
89	aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909
90	Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn	
91	215 220 225	
93	cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957
94	Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro	
95	230 235 240	
97	cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005
98	Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu	
99	245 250 255 260	
101	gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053
102	Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn	
103	265 270 275	
105	tac tgc gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101
106	Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe	
107	280 285 290	
109	ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149
110	Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys	
111	295 300 305	
113	gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg	1197
114	Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val	
115	310 315 320	
117	aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg	1245
118	Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg	
119	325 330 335 340	
121	agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac	1293
122	Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His	
123	345 350 355	
125	cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa	1338

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126 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
127          360          365          370
129 gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat 1398
130 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
131 agtgggttgc gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
132 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga gggtatatat 1578
133 gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt 1638
134 ttttgggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
135 tcctttgcca aaataaggga tgggtcaaata tatgaaacat gtcttttagaa aatttaggag 1758
136 ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818
137 agcatcttgt atattaaaaa tcaaaagatg aggcctttctt acatatacat cttagttgat 1878
138 tatt 1882
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 370
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2
146 Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
147 1 5 10 15
148 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
149 20 25 30
150 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
151 35 40 45
152 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
153 50 55 60
154 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
155 65 70 75 80
156 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
157 85 90 95
158 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
159 100 105 110
160 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
161 115 120 125
162 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
163 130 135 140
164 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
165 145 150 155 160
166 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
167 165 170 175
168 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
169 180 185 190
170 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
171 195 200 205
173 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
174 210 215 220
175 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
176 225 230 235 240
177 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
178 245 250 255

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179 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
180          260          265          270
181 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
182          275          280          285
183 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
184          290          295          300
185 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
186          305          310          315          320
187 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
188          325          330          335
189 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
190          340          345          350
191 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
192          355          360          365
193 Pro Arg
194          370
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1472
198 <212> TYPE: DNA
199 <213> ORGANISM: Mus musculus
201 <220> FEATURE:
202 <221> NAME/KEY: CDS
203 <222> LOCATION: (93)...(1205)
205 <400> SEQUENCE: 3
206 agggactgtg cagtagaaat ccgccgactc aacccttttg gctttattta tttacttttg      60
207 gagcaacgcg atccctaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc      113
208                               Met Gln Arg Leu Val Leu Val
209                               1          5
211 tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg      161
212 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
213          10          15          20
216 act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg      209
217 Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
218          25          30          35
220 aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac      257
221 Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
222          40          45          50          55
224 att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac      305
225 Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
226          60          65          70
228 agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag      353
229 Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu
230          75          80          85
232 aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa      401
233 Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu
234          90          95          100
236 gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc      449
237 Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu Val
238          105          110          115

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240	tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag	497
241	Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu	
242	120 125 130 135	
244	atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt	545
245	Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe	
246	140 145 150	
248	aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat	593
249	Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr	
250	155 160 165	
252	tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg	641
253	Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp	
254	170 175 180	
256	gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca	689
257	Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser	
258	185 190 195	
261	ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca	737
262	Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala	
263	200 205 210 215	
265	gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct	785
266	Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser	
267	220 225 230	
269	tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga	833
270	Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg	
271	235 240 245	
273	ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc	881
274	Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu	
275	250 255 260	
277	aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg	929
278	Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val	
279	265 270 275	
281	aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga	977
282	Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg	
283	280 285 290 295	
285	tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc	1025
286	Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val	
287	300 305 310	
289	aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat	1073
290	Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr	
291	315 320 325	
293	cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa	1121
294	His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys	
295	330 335 340	
297	gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga	1169
298	Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg	
299	345 350 355	
302	tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc	1215
303	Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *	
304	360 365 370	
306	acatctgtac tttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa	1275

VERIFICATION SUMMARY

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Input Set : A:\00-100.txt

Output Set: N:\CRF3\07022002\J039847A.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date